Claims

1. Method for the subtype-independent and/or species-independent detection of nucleic acids of HI viruses in a sample by hybridizing the nucleic acids with an oligonucleotide combination comprising two or more oligonucleotides which hybridize specifically with HIV nucleic acids and contain in each case 10 to 80 consecutive nucleotides from
   (i) the same highly conserved region of the LTR region, of the *gag* gene or of the *pol* gene of HIV represented by one of the sequences shown in SEQ ID NO: 1 to 13,
   (ii) a corresponding region of another HI virus isolate,
   (iii) a corresponding region of a consensus sequence derived from several HI virus isolates

   or sequences which are complementary thereto, and carrying out an enzymatic amplification step.

2. Method as claimed in claim 1,
   wherein
   it comprises the steps:
   (a) contacting a sample with the oligonucleotides under such conditions that the oligonucleotides hybridize with the HIV nucleic acids from HIV-1 or/and HIV-2 that are present in the sample,
   (b) determining the presence and/or the amount of HIV nucleic acids in the sample.

3. Method as claimed in claim 1 or 2,
wherein
only a single oligonucleotide combination is used.

4. Method as claimed in one of the claims 1 to 3,
wherein
the oligonucleotides are selected for a subtype-independent detection in such a manner that at least 7 of the HIV-1 subtypes selected from the subtypes A, B, C, D, E, F, G, H and O and at least 2 of the HIV-2 subtypes selected from the subtypes A, B, C and D are detected.

5. Method as claimed in one of the claims 1 to 3,
wherein
the oligonucleotides are selected for a species-independent detection in such a manner that at least 7 of the HIV-1 subtypes selected from the subtypes A, B, C, D, E, F, G, H and O and additionally at least one of the HIV-2 subtypes selected from the subtypes A, B, C and D are detected.

6. Method for the subtype-independent and/or species-independent detection of nucleic acids of HI viruses in a sample by hybridizing the nucleic acids with two or more oligonucleotide combinations, each oligonucleotide combination comprising a first oligonucleotide which comprises 10 to 80 consecutive nucleotides from

(i) a highly conserved region of the LTR region, of the *gag* gene or of the *pol* gene of HIV represented by one of the sequences shown in SEQ ID NO: 1 to 13,

(ii) a corresponding region of another HI virus isolate ,

(iii) a corresponding region of a consensus sequence derived from several HI virus isolates,

or sequences which are complementary thereto, and a second oligonucleotide which enables subtype-specific and/or species-specific hybridization with HIV nucleic acids, and carrying out an enzymatic amplification step, wherein the entirety of the oligonucleotide combinations allows a subtype-independent and/or species-independent detection of HI viruses.

7. Method as claimed in claim 6,
wherein
the oligonucleotides are selected for the subtype-independent detection in such a manner that at least 7 of the HIV-1 subtypes selected from the subtypes A, B, C, D, E, F, G, H and O and at least 2 of the HIV-2 subtypes selected from the subtypes A, B, C and D are detected.

8. Method as claimed in claim 7,
wherein
at least two oligonucleotides are used for the detection which contain in each case 10 to 80 consecutive nucleotides from

(i) a highly conserved region of the LTR gene, of the *gag* gene or of the *pol* gene of HIV represented by one of the sequences shown in SEQ ID NO: 2, 4, 5, 6, 8, 9, 10, 12 and 13,

(ii) a corresponding region of another HI virus isolate ,

(iii) a corresponding region of a consensus sequence derived from several HI virus isolates

or sequences which are complementary thereto.

9. Method as claimed in claim 6,
wherein
the oligonucleotides are selected for the species-independent detection in such a manner that at least 7 of the HIV-1 subtypes selected from the subtypes A, B, C, D, E, F, G, H and O and additionally at least one of the HIV-2 subtypes selected from the subtypes A, B, C and D are detected.

10. Method as claimed in claim 9,
wherein
at least two oligonucleotides are used for the detection which contain in each case 10 to 80 consecutive nucleotides from
(i) a highly conserved region of the LTR gene, of the *gag* gene or of the *pol* gene of HIV represented by one of the sequences shown in SEQ ID NO: 1, 2, 3, 4, 5, 7, 9, 10 and 13,
(ii) a corresponding region of another HI virus isolate,
(iii) a corresponding region of a consensus sequence derived from several HI virus isolates
or sequences which are complementary thereto.

11. Method as claimed in one of the previous claims,
wherein
the oligonucleotides have or contain the sequences shown in SEQ ID NO. 14 to 25.

12. Method as claimed in one of the previous claims, **wherein**
at least one oligonucleotide has one or several labels.

13. Oligonucleotide,
wherein
it comprises 10 to 80 consecutive nucleotides from
(i) a highly conserved region of the *pol* gene of HIV represented by one of the sequences shown in SEQ ID NO: 4, 5, 9 or 10,
(ii) a corresponding region of another HI virus isolate,
(iii) a corresponding region of a consensus sequence derived from several HI virus isolates
or sequences which are complementary thereto,
provided that it does not comprise the nucleotide sequence
CTACTACTCC TTGACTTTGG GGATTG
or its complementary sequence.

14. Oligonucleotide as claimed in claim 13,
wherein
it comprises 10 to 80 consecutive nucleotides from
(i) a highly conserved region of the *pol* gene of HIV represented by one of the sequences shown in SEQ ID NO: 4, 5 or 9,
(ii) a corresponding region of another HI virus isolate,
(iii) a corresponding region of a consensus sequence derived from several HI virus isolates
or sequences which are complementary thereto.

15. Oligonucleotide,
wherein
it comprises at least one of the sequences shown in SEQ ID NO. 14, 16, 17, 18, 20, 22, 23, 24 and 25.

16. Oligonucleotide as claimed in one of the claims 13 to 15,
wherein
it has no mismatches at its 3' end with nucleic acids of the subtypes A, B, C, D, E, F, G, H and O of HIV-1 and of the subtypes A, B, C and D of HIV-2.

17. Oligonucleotide as claimed in one of the claims 13 to 16,
wherein
it has one or several labels.

18. Combination of several oligonucleotides comprising at least two oligonucleotides,
wherein
the at least two oligonucleotides each comprise 10 to 80 consecutive nucleotides from
(i) a highly conserved region of the LTR region, of the *gag* gene or of the *pol* gene of HIV represented by one of the sequences shown in SEQ ID NO: 1 to 13,
(ii) a corresponding region of another HI virus isolate,
(iii) a corresponding region of a consensus sequence derived from several HI virus isolates

or sequences which are complementary thereto and the combination is selected such that it allows an enzymatic amplification.

19. Combination of several oligonucleotides comprising at least two oligonucleotides selected from the oligonucleotides as claimed in one of the claims 13 to 17 and optionally additional oligonucleotides which each contain a sequence that is specific for a single subtype of HIV-1 and/or HIV-2, wherein the entirety of the oligonucleotides allows a subtype-independent and/or species-independent detection of HI viruses.

20. Reagent kit comprising an oligonucleotide as claimed in one of the claims 13 to 17 or an oligonucleotide combination as claimed in claim 18 or 19 as primers and/or probes for the detection of HI viruses or their nucleic acids and suitable means for carrying out a hybridization and amplification of nucleic acids in a sample.

21. Use of oligonucleotides or oligonucleotide combinations as claimed in one of the claims 13 to 19 as primers and/or probes for the subtype-independent and/or species-independent detection of HI viruses.